Pak

1646

CRF Errors Corrected by the STIC System Branch

ENTERED   RECEIVED

SEP 14 2000

TECH CENTER 1600/2900

Serial Number: 09/039,927A

CRF Processing Date: 9/8/2000

Edited by: _____

Verified by: _____ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically:
_____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
_____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____ .

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☑ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other:
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

M.Pak

1646

```
RAW SEQUENCE LISTING              DATE: 09/08/2000
PATENT APPLICATION:  US/09/039,927A     TIME: 12:15:07

Input Set : A:\A63098.app
Output Set: N:\CRF3\09082000\I039927A.raw
```

Does Not Comply
Corrected Diskette Needed

```
            SEQUENCE LISTING
     4 (1) GENERAL INFORMATION:
     6        (i) APPLICANT: Lester, Henry A.
     7                       Davidson, Norman
     8                       Kofuji, Paulo
    10       (ii) TITLE OF INVENTION: INWARD RECTIFIER, G-PROTEIN ACTIVATED,
    11                       MAMMALIAN, POTASSIUM CHANNELS AND USES THEREOF
    13      (iii) NUMBER OF SEQUENCES: 6
    15       (iv) CORRESPONDENCE ADDRESS:
    16            (A) ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
    17            (B) STREET: Four Embarcadero Center, Suite 3400
    18            (C) CITY: San Francisco
    19            (D) STATE: California
    20            (E) COUNTRY: United States
    21            (F) ZIP: 94111-4187
    23        (v) COMPUTER READABLE FORM:
    24            (A) MEDIUM TYPE: Floppy disk
    25            (B) COMPUTER: IBM PC compatible
    26            (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    27            (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
    29       (vi) CURRENT APPLICATION DATA:
C--> 30            (A) APPLICATION NUMBER: US/09/039,927A
C--> 31            (B) FILING DATE: 16-Mar-1998
    32            (C) CLASSIFICATION:
    38      (vii) PRIOR APPLICATION DATA:
    35            (A) APPLICATION NUMBER: US 08/066,371
    36            (B) FILING DATE: 21-MAR-1993
    39            (A) APPLICATION NUMBER: US 08/614,801
    40            (B) FILING DATE: 07-MAR-1996
    42     (viii) ATTORNEY/AGENT INFORMATION:
    43            (A) NAME: Trecartin, Richard F.
    44            (B) REGISTRATION NUMBER: 31,801
    45            (C) REFERENCE/DOCKET NUMBER: A-63098-1/RFT
    47       (ix) TELECOMMUNICATION INFORMATION:
    48            (A) TELEPHONE: (415) 781-1989
    49            (B) TELEFAX: (415) 398-3249
    50            (C) TELEX: 910 277299


ERRORED SEQUENCES

   470 (2) INFORMATION FOR SEQ ID NO: 4:
   472        (i) SEQUENCE CHARACTERISTICS:
   473            (A) LENGTH: 414 amino acids
   474            (B) TYPE: amino acid
   475            (D) TOPOLOGY: linear
   477       (ii) MOLECULE TYPE: protein
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RAW SEQUENCE LISTING   DATE: 09/08/2000
PATENT APPLICATION: US/09/039,927A   TIME: 12:15:07

Input Set : A:\A63098.app
Output Set: N:\CRF3\09082000\I039927A.raw

```
      479    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
      481    Met Thr Met Ala Lys Leu Thr Glu Ser Met Thr Asn Val Leu Glu Gly
      482    1               5                   10                  15
      484    Asp Ser Met Asp Gln Asp Val Glu Ser Pro Val Ala Ile His Gln Pro
      485                20                  25                  30
      487    Lys Leu Pro Lys Gln Ala Arg Asp Asp Leu Pro Arg His Ile Ser Arg
      488                35                  40                  45
      490    Asp Arg Thr Lys Arg Lys Ile Gln Arg Tyr Val Arg Lys Asp Gly Lys
      491                50                  55                  60
      493    Cys Asn Val His His Gly Asn Val Arg Glu Thr Tyr Arg Tyr Leu Thr
      494    65                  70                  75                  80
      496    Asp Ile Phe Thr Thr Leu Val Asp Leu Lys Trp Arg Phe Asn Leu Leu
      497                85                  90                  95
      499    Ile Phe Val Met Val Tyr Thr Val Thr Trp Leu Phe Phe Gly Met Ile
      500                100                 105                 110
      502      Trp Trp Leu Ile Ala Tyr Ile Arg Gly Asp Met Asp His Ile Glu Asp
E--> 503              115                 120                 125
      505    Pro Ser Trp Thr Pro Cys Val Thr Asn Leu Asn Gly Phe Val Ser Ala
E--> 506                130                 135                 140
      508    Phe Leu Phe Ser Ile Glu Thr Glu Thr Thr Ile Gly Tyr Gly Tyr Arg
E--> 509    145                 150                 155                 160
      511    Val Ile Thr Asp Lys Cys Pro Glu Gly Ile Ile Leu Leu Leu Ile Gln
E--> 512                165                 170                 175
      514    Ser Val Leu Gly Ser Ile Val Asn Ala Phe Met Val Gly Cys Met Phe
E--> 515                180                 185                 190
      517    Val Lys Ile Ser Gln Pro Lys Lys Arg Ala Glu Thr Leu Val Phe Ser
E--> 518                195                 200                 205
      520    Thr His Ala Val Ile Ser Met Arg Asp Gly Lys Leu Cys Leu Met Phe
E--> 521                210                 215                 220
      523    Arg Val Gly Asp Leu Arg Asn Ser His Ile Val Glu Ala Ser Ile Arg
E--> 524    225                 230                 235                 240
      526    Ala Lys Leu Ile Lys Ser Lys Gln Thr Ser Glu Gly Glu Phe Ile Pro
E--> 527                245                 250                 255
      529    Leu Asn Gln Ser Asp Ile Asn Val Gly Tyr Tyr Thr Gly Asp Asp Arg
E--> 530                260                 265                 270
      532    Leu Phe Leu Val Ser Pro Leu Ile Ile Ser His Glu Ile Asn Gln Gln
E--> 533                275                 280                 285
      535    Ser Pro Phe Trp Glu Ile Ser Lys Ala Gln Leu Pro Lys Glu Glu Leu
E--> 536                290                 295                 300
      538    Glu Ile Val Val Ile Leu Glu Gly Ile Val Glu Ala Thr Gly Met Thr
E--> 539    305                 310                 315                 320
      541    Cys Gln Ala Arg Ser Ser Tyr Ile Thr Ser Glu Ile Leu Trp Gly Tyr
E--> 542                325                 330                 335
      544    Arg Phe Thr Pro Val Leu Thr Met Glu Asp Gly Phe Tyr Glu Val Asp
E--> 545                340                 345                 350
      547    Tyr Asn Ser Phe His Glu Thr Tyr Glu Thr Ser Thr Pro Ser Leu Ser
E--> 548                355                 360                 365
      550    Ala Lys Glu Leu Ala Glu Leu Ala Asn Arg Ala Glu Val Pro Leu Ser
E--> 551                370                 375                 380
```

RAW SEQUENCE LISTING   DATE: 09/08/2000
PATENT APPLICATION: US/09/039,927A   TIME: 12:15:07

Input Set : A:\A63098.app
Output Set: N:\CRF3\09082000\I039927A.raw

```
       553   Trp Ser Val Ser Ser Lys Leu Asn Gln His Ala Glu Leu Glu Thr Glu
E--> 554   385                 390                 395                 400
       556   Glu Glu Glu Lys Asn Pro Glu Glu Leu Thr Glu Arg Asn Gly
E--> 557                       405                 410
```

VERIFICATION SUMMARY   DATE: 09/08/2000
PATENT APPLICATION: US/09/039,927A   TIME: 12:15:08

Input Set : A:\A63098.app
Output Set: N:\CRF3\09082000\I039927A.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:503 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4

RAW SEQUENCE LISTING   DATE: 09/12/2000
PATENT APPLICATION: US/09/039,927A   TIME: 10:36:12

Input Set : A:\Pto.amc
Output Set: N:\CRF3\09122000\I039927A.raw

SEQUENCE LISTING

```
    4 (1) GENERAL INFORMATION:
    6       (i) APPLICANT: Lester, Henry A.
    7                      Davidson, Norman
    8                      Kofuji, Paulo
   10      (ii) TITLE OF INVENTION: INWARD RECTIFIER, G-PROTEIN ACTIVATED,
   11                              MAMMALIAN, POTASSIUM CHANNELS AND USES THEREOF
   13     (iii) NUMBER OF SEQUENCES: 6
   15      (iv) CORRESPONDENCE ADDRESS:
   16          (A) ADDRESSEE: Flehr Hohbach Test Albritton & Herbert LLP
   17          (B) STREET: Four Embarcadero Center, Suite 3400
   18          (C) CITY: San Francisco
   19          (D) STATE: California
   20          (E) COUNTRY: United States
   21          (F) ZIP: 94111-4187
   23      (v) COMPUTER READABLE FORM:
   24          (A) MEDIUM TYPE: Floppy disk
   25          (B) COMPUTER: IBM PC compatible
   26          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
   27          (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
   29      (vi) CURRENT APPLICATION DATA:
C-->30          (A) APPLICATION NUMBER: US/09/039,927A
C-->31          (B) FILING DATE: 16-Mar-1998
   32          (C) CLASSIFICATION:
   38     (vii) PRIOR APPLICATION DATA:
   35          (A) APPLICATION NUMBER: US 08/066,371
   36          (B) FILING DATE: 21-MAR-1993
   39          (A) APPLICATION NUMBER: US 08/614,801
   40          (B) FILING DATE: 07-MAR-1996
   42    (viii) ATTORNEY/AGENT INFORMATION:
   43          (A) NAME: Trecartin, Richard F.
   44          (B) REGISTRATION NUMBER: 31,801
   45          (C) REFERENCE/DOCKET NUMBER: A-63098-1/RFT
   47      (ix) TELECOMMUNICATION INFORMATION:
   48          (A) TELEPHONE: (415) 781-1989
   49          (B) TELEFAX: (415) 398-3249
   50          (C) TELEX: 910 277299
   52 (2) INFORMATION FOR SEQ ID NO: 1:
   54      (i) SEQUENCE CHARACTERISTICS:
   55          (A) LENGTH: 2070 base pairs
   56          (B) TYPE: nucleic acid
   57          (C) STRANDEDNESS: unknown
   58          (D) TOPOLOGY: unknown
   60     (ii) MOLECULE TYPE: DNA (genomic)
   63     (ix) FEATURE:
   64          (A) NAME/KEY: CDS
   65          (B) LOCATION: 32..1534
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Input Set : A:\Pto.amc
Output Set: N:\CRF3\09122000\I039927A.raw

```
67    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:                                52
69    GGCACGAGAA TCTGGATCTC CCCTCCGTAT T ATG TCT GCA CTC CGA AGG AAA
70                                          Met Ser Ala Leu Arg Arg Lys
                                              1                   5
71
73    TTT GGG GAC GAT TAC CAG GTA GTG ACC ACT TCG TCC AGC GGT TCG GGC       100
74    Phe Gly Asp Asp Tyr Gln Val Val Thr Thr Ser Ser Ser Gly Ser Gly
75                 10              15                  20
77    TTG. CAG CCC CAG GGG CCA GGA CAG GGC CCA CAG CAG CAG CTT GTA CCC       148
78    Leu Gln Pro Gln Gly Pro Gly Gln Gly Pro Gln Gln Gln Leu Val Pro
79                 25              30                  35
81    AAG AAG AAA CGG CAG CGG TTC GTG GAC AAG AAC GGT CGG TGC AAT GTG       196
82    Lys Lys Lys Arg Gln Arg Phe Val Asp Lys Asn Gly Arg Cys Asn Val
83    40              45                  50                  55
85    CAG CAC GGC AAC CTG GGC AGC GAG ACC AGT CGC TAC CTT TCC GAC CTC       244
86    Gln His Gly Asn Leu Gly Ser Glu Thr Ser Arg Tyr Leu Ser Asp Leu
87                 60                  65                  70
89    TTC ACT ACC CTG GTG GAT CTC AAG TGG CGT TGG AAC CTC TTT ATC TTC       292
90    Phe Thr Thr Leu Val Asp Leu Lys Trp Arg Trp Asn Leu Phe Ile Phe
91                 75                  80                  85
93    ATC CTC ACC TAC ACC GTG GCC TGG CTC TTC ATG GCG TCC ATG TGG TGG       340
94    Ile Leu Thr Tyr Thr Val Ala Trp Leu Phe Met Ala Ser Met Trp Trp
95                 90                  95                  100
97    GTG ATC GCT TAT ACC CGG GGC GAC CTG AAC AAA GCC CAT GTC GGC AAC       388
98    Val Ile Ala Tyr Thr Arg Gly Asp Leu Asn Lys Ala His Val Gly Asn
99    105                 110                 115
101   TAC ACT CCC TGT GTG GCC AAT GTC TAT AAC TTC CCC TCT GCC TTC CTT       436
102   Tyr Thr Pro Cys Val Ala Asn Val Tyr Asn Phe Pro Ser Ala Phe Leu
103   120             125                 130                 135
105   TTC TTC ATC GAG ACC GAG GCC ACC ATC GGC TAT GGC TAC CGC TAC ATC       484
106   Phe Phe Ile Glu Thr Glu Ala Thr Ile Gly Tyr Gly Tyr Arg Tyr Ile
107                   140                 145                 150
109   ACC GAC AAG TGC CCC GAG GGC ATC ATC CTT TTC CTT TTC CAG TCC ATC       532
110   Thr Asp Lys Cys Pro Glu Gly Ile Ile Leu Phe Leu Phe Gln Ser Ile
111           155                 160                 165
113   CTT GGC TCC ATC GTG GAC GCT TTC CTC ATC GGC TGC ATG TTC ATC AAG       580
114   Leu Gly Ser Ile Val Asp Ala Phe Leu Ile Gly Cys Met Phe Ile Lys
115                 170                 175                 180
117   ATG TCC CAG CCC AAA AAG CGC GCC GAG ACC CTC ATG TTT AGC GAG CAT       628
118   Met Ser Gln Pro Lys Lys Arg Ala Glu Thr Leu Met Phe Ser Glu His
119           185                 190                 195
121   GCG GTT ATT TCC ATG AGG GAC GGA AAA CTC ACT CTC ATG TTC CGG GTG       676
122   Ala Val Ile Ser Met Arg Asp Gly Lys Leu Thr Leu Met Phe Arg Val
123   200             205                 210                 215
125   GGC AAC CTG CGC AAC AGC CAC ATG GTC TCC GCG CAG ATC CGC TGC AAG       724
126   Gly Asn Leu Arg Asn Ser His Met Val Ser Ala Gln Ile Arg Cys Lys
127                 220                 225                 230
129   CTG CTC AAA TCT CGG CAG ACA CCT GAG GGT GAG TTT CTA CCC CTT GAC       772
130   Leu Leu Lys Ser Arg Gln Thr Pro Glu Gly Glu Phe Leu Pro Leu Asp
131                 235                 240                 245
```

RAW SEQUENCE LISTING   DATE: 09/12/2000
PATENT APPLICATION: US/09/039,927A   TIME: 10:36:12

        Input Set : A:\Pto.amc
        Output Set: N:\CRF3\09122000\I039927A.raw

```
133    CAA CTT GAA CTG GAT GTA GGT TTT AGT ACA GGG GCA GAT CAA CTT TTT       820
134    Gln Leu Glu Leu Asp Val Gly Phe Ser Thr Gly Ala Asp Gln Leu Phe
135            250                 255                 260
137    CTT GTG TCC CCT CTC ACC ATT TGC CAC GTG ATC GAT GCC AAA AGC CCC       868
138    Leu Val Ser Pro Leu Thr Ile Cys His Val Ile Asp Ala Lys Ser Pro
139            265                 270                 275
141    TTT TAT GAC CTA TCC CAG CGA AGC ATG CAA ACT GAA CAG TTC GAG GTG       916
142    Phe Tyr Asp Leu Ser Gln Arg Ser Met Gln Thr Glu Gln Phe Glu Val
143    280                 285                 290                 295
145    GTC GTC ATC CTG GAA GGC ATC GTG GAA ACC ACA GGG ATG ACT TGT CAA       964
146    Val Val Ile Leu Glu Gly Ile Val Glu Thr Thr Gly Met Thr Cys Gln
147            300                 305                 310
149    GCT CGA ACA TCA TAC ACC GAA GAT GAA GTT CTT TGG GGT CAT CGT TTT      1012
150    Ala Arg Thr Ser Tyr Thr Glu Asp Glu Val Leu Trp Gly His Arg Phe
151            315                 320                 325
153    TTC CCT GTA ATT TCT TTA GAA GAA GGA TTC TTT AAA GTC GAT TAC TCC      1060
154    Phe Pro Val Ile Ser Leu Glu Glu Gly Phe Phe Lys Val Asp Tyr Ser
155            330                 335                 340
157    CAG TTC CAT GCA ACC TTT GAA GTC CCC ACC CCT CCG TAC AGT GTG AAA      1108
158    Gln Phe His Ala Thr Phe Glu Val Pro Thr Pro Pro Tyr Ser Val Lys
159         345                 350                 355
161    GAG CAG GAA GAA ATG CTT CTC ATG TCT TCC CCT TTA ATA GCA CCA GCC      1156
162    Glu Gln Glu Glu Met Leu Leu Met Ser Ser Pro Leu Ile Ala Pro Ala
163    360                 365                 370                 375
165    ATA ACC AAC AGC AAA GAA AGA CAC AAT TCT GTG GAG TGC TTA GAT GGA      1204
166    Ile Thr Asn Ser Lys Glu Arg His Asn Ser Val Glu Cys Leu Asp Gly
167            380                 385                 390
169    CTA GAT GAC ATT AGC ACA AAA CTT CCA TCG AAG CTG CAG AAA ATT ACG      1252
170    Leu Asp Asp Ile Ser Thr Lys Leu Pro Ser Lys Leu Gln Lys Ile Thr
171            395                 400                 405
173    GGG AGA GAA GAC TTT CCC AAA AAA CTC CTG AGG ATG AGT TCT ACA ACT      1300
174    Gly Arg Glu Asp Phe Pro Lys Lys Leu Leu Arg Met Ser Ser Thr Thr
175            410                 415                 420
177    TCA GAA AAA GCC TAT AGT TTG GGT GAT TTG CCC ATG AAA CTC CAA CGA      1348
178    Ser Glu Lys Ala Tyr Ser Leu Gly Asp Leu Pro Met Lys Leu Gln Arg
179         425                 430                 435
181    ATA AGT TCG GTT CCT GGC AAC TCT GAA GAA AAA CTG GTA TCT AAA ACC      1396
182    Ile Ser Ser Val Pro Gly Asn Ser Glu Glu Lys Leu Val Ser Lys Thr
183    440                 445                 450                 455
185    ACC AAG ATG TTA TCA GAT CCC ATG AGC CAG TCT GTG GCC GAT TTG CCA      1444
186    Thr Lys Met Leu Ser Asp Pro Met Ser Gln Ser Val Ala Asp Leu Pro
187            460                 465                 470
189    CCG AAG CTT CAA AAG ATG GCT GGA GGA CCT ACC AGG ATG GAA GGG AAT      1492
190    Pro Lys Leu Gln Lys Met Ala Gly Gly Pro Thr Arg Met Glu Gly Asn
191            475                 480                 485
193    CTT CCA GCC AAA CTA AGA AAA ATG AAC TCT GAC CGC TTC ACA             1534
194    Leu Pro Ala Lys Leu Arg Lys Met Asn Ser Asp Arg Phe Thr
195         490                 495                 500
197    TAGCAAAACA CCCCATTAGG CATTATTTCA TGTTTTGATT TAGTTTTAGT CCAATATTTG    1594
```

RAW SEQUENCE LISTING   DATE: 09/12/2000
PATENT APPLICATION: US/09/039,927A   TIME: 10:36:12

Input Set : A:\Pto.amc
Output Set: N:\CRF3\09122000\I039927A.raw

```
199   GCTGATAAGA TAATCCTCCC CGGGAAATCT GAGAGGTCTA TCCCAGTCTG GCAAATTCAT   1654
201   CAGAGGACTC TTCATTGAAG TGTTGTTACT GTGTTGAACA TGAGTTACAA AGGGAGGACA   1714
203   TCATAAGAAA GCTAATAGTT GGCATGTATT ATCACATCAA GCATGCAATA ATGTGCAAAT   1774
205   TTTGCATTTA GTTTTCTGGC ATGATTTATA TATGGCATAT TTATATTGAA TATTCTGGAA   1834
207   AAATATATAA ATATATATTT GAAGTGGAGA TATTCTCCCC ATAATTTCTA ATATATGTAT   1894
209   TAAGCCAAAC ATGAGTGGAT AGCTTTCAGG GCACTAAAAT AATATACATG CATACATACA   1954
211   TACATGCATA TGCACAGACA CATACACACA CATACTCATA TATATAAAAC ATACCCATAC   2014
213   AAACATATAT ATCTAATAAA AATTGTGATG TTTTGTTCAA AAAAAAAAAA AAAAAA       2070
```

216 (2) INFORMATION FOR SEQ ID NO: 2:
218   (i) SEQUENCE CHARACTERISTICS:
219   (A) LENGTH: 501 amino acids
220   (B) TYPE: amino acid
221   (D) TOPOLOGY: linear
223   (ii) MOLECULE TYPE: protein
225   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
227   Met Ser Ala Leu Arg Arg Lys Phe Gly Asp Asp Tyr Gln Val Val Thr
228    1               5                  10                  15
230   Thr Ser Ser Ser Gly Ser Gly Leu Gln Pro Gln Gly Pro Gly Gln Gly
231                   20                  25                  30
233   Pro Gln Gln Gln Leu Val Pro Lys Lys Lys Arg Gln Arg Phe Val Asp
234                   35                  40                  45
236   Lys Asn Gly Arg Cys Asn Val Gln His Gly Asn Leu Gly Ser Glu Thr
237    50                  55                  60
239   Ser Arg Tyr Leu Ser Asp Leu Phe Thr Thr Leu Val Asp Leu Lys Trp
240    65                  70                  75                  80
242   Arg Trp Asn Leu Phe Ile Phe Ile Leu Thr Tyr Thr Val Ala Trp Leu
243                       85                  90                  95
245   Phe Met Ala Ser Met Trp Trp Val Ile Ala Tyr Thr Arg Gly Asp Leu
246                   100                 105                 110
248   Asn Lys Ala His Val Gly Asn Tyr Thr Pro Cys Val Ala Asn Val Tyr
249                   115                 120                 125
251   Asn Phe Pro Ser Ala Phe Leu Phe Phe Ile Glu Thr Glu Ala Thr Ile
252                   130                 135                 140
254   Gly Tyr Gly Tyr Arg Tyr Ile Thr Asp Lys Cys Pro Glu Gly Ile Ile
255    145                 150                 155                 160
257   Leu Phe Leu Phe Gln Ser Ile Leu Gly Ser Ile Val Asp Ala Phe Leu
258                   165                 170                 175
260   Ile Gly Cys Met Phe Ile Lys Met Ser Gln Pro Lys Lys Arg Ala Glu
261                   180                 185                 190
263   Thr Leu Met Phe Ser Glu His Ala Val Ile Ser Met Arg Asp Gly Lys
264                   195                 200                 205
266   Leu Thr Leu Met Phe Arg Val Gly Asn Leu Arg Asn Ser His Met Val
267    210                 215                 220
269   Ser Ala Gln Ile Arg Cys Lys Leu Leu Lys Ser Arg Gln Thr Pro Glu
270    225                 230                 235                 240
272   Gly Glu Phe Leu Pro Leu Asp Gln Leu Glu Leu Asp Val Gly Phe Ser
273                   245                 250                 255
275   Thr Gly Ala Asp Gln Leu Phe Leu Val Ser Pro Leu Thr Ile Cys His
276                   260                 265                 270
```

RAW SEQUENCE LISTING   DATE: 09/12/2000
PATENT APPLICATION: US/09/039,927A   TIME: 10:36:12

Input Set : A:\Pto.amc
Output Set: N:\CRF3\09122000\I039927A.raw

```
278     Val Ile Asp Ala Lys Ser Pro Phe Tyr Asp Leu Ser Gln Arg Ser Met
279             275                 280                 285
281     Gln Thr Glu Gln Phe Glu Val Val Ile Leu Glu Gly Ile Val Glu
282             290                 295             300
284     Thr Thr Gly Met Thr Cys Gln Ala Arg Thr Ser Tyr Thr Glu Asp Glu
285     305                 310                 315                 320
287     Val Leu Trp Gly His Arg Phe Phe Pro Val Ile Ser Leu Glu Glu Gly
288                     325                 330                 335
290     Phe Phe Lys Val Asp Tyr Ser Gln Phe His Ala Thr Phe Glu Val Pro
291             340                 345                 350
293     Thr Pro Pro Tyr Ser Val Lys Glu Gln Glu Glu Met Leu Leu Met Ser
294             355                 360                 365
296     Ser Pro Leu Ile Ala Pro Ala Ile Thr Asn Ser Lys Glu Arg His Asn
297             370                 375                 380
299     Ser Val Glu Cys Leu Asp Gly Leu Asp Asp Ile Ser Thr Lys Leu Pro
300     385                 390                 395                 400
302     Ser Lys Leu Gln Lys Ile Thr Gly Arg Glu Asp Phe Pro Lys Lys Leu
303                     405                 410                 415
305     Leu Arg Met Ser Ser Thr Thr Ser Glu Lys Ala Tyr Ser Leu Gly Asp
306             420                 425                 430
308     Leu Pro Met Lys Leu Gln Arg Ile Ser Ser Val Pro Gly Asn Ser Glu
309             435                 440                 445
311     Glu Lys Leu Val Ser Lys Thr Thr Lys Met Leu Ser Asp Pro Met Ser
312             450                 455                 460
314     Gln Ser Val Ala Asp Leu Pro Pro Lys Leu Gln Lys Met Ala Gly Gly
315     465                 470                 475                 480
317     Pro Thr Arg Met Glu Gly Asn Leu Pro Ala Lys Leu Arg Lys Met Asn
318                     485                 490                 495
320     Ser Asp Arg Phe Thr
321             500
323 (2) INFORMATION FOR SEQ ID NO: 3:
325     (i) SEQUENCE CHARACTERISTICS:
326             (A) LENGTH: 1978 base pairs
327             (B) TYPE: nucleic acid
328             (C) STRANDEDNESS: unknown
329             (D) TOPOLOGY: unknown
331     (ii) MOLECULE TYPE: DNA (genomic)
333     (ix) FEATURE:
334             (A) NAME/KEY: CDS
335             (B) LOCATION: 488..1729
337     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
339     GTCTCCCTGC AAGGTCTATC ACTTTGCTCC TAAACGAGGA TTTATTCCCT CTGCCACTCA      60
341     AGGCTGTCCC CCAGTTTCCT CGCAACCGGG CTTCCTCCTC AGTCCCTGCC CACACGCGCA     120
343     CTCCTCTGCC CCGCGGTGGC CCCAGCGCCC AGCCCTCCAG CCAGAGGGAG CCAGGCACCA     180
345     GACGGCAGCA CCTGGCTGGA GAGGTTGGGC GGGCCGAGGG TGGGGATCCG CGGGAACCGG     240
347     CGAGTCGGAG CTGGAGCAGG AGCTGGACCC AACCGCTAGC AGCAGAATGG AGTCTCCTGA     300
349     AAGCCTGCCG GGGCTGATGT GAAATTGGGC CATCTGCTTC CAGTTGGTCT GTTTCCTCCT     360
351     TTTCTTGTAT TTTCTTCCCT CGCCATTCAC CGTGGAGTGA ATTATTGAAT CTTGCTCCGT     420
353     TCCGAGAGAG GCGATCAGGA TGGAGTGAAC CTACCCTGTC CACTACAAGG AAAAGCACAA     480
```

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/039,927A

DATE: 09/12/2000
TIME: 10:36:13

Input Set : A:\Pto.amc
Output Set: N:\CRF3\09122000\I039927A.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]